

Genotype variation in duplicate accessions of heirloom tomatoes (*Lycopersicon esculentum*) using 8 microsatellite markers

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Eliminating unintentional duplication of germplasm in genebanks will allow more resources to be devoted towards acquiring new material, characterizing accessions, and routine regenerations. Based on passport data, we suspect that 15% or more of the nearly 6,000 accessions of tomato at PGRU may be unwanted duplicates. In a pilot study to estimate redundancy, two heirloom tomato cultivars were assessed for molecular genetic variation within and among accessions. Two plants from each of six accessions of San Marzano and six accessions of Globe were genotyped at 8 microsatellite loci distributed across the genome. An Analysis of Molecular Variance (AMOVA) was used to partition the genetic variation among plants within accessions, among accessions, and among cultivars. Results from this study will be used in designing a sampling strategy to genotype the 200-300 accessions of American Heirlooms in PGRU's collection. Combined genotypic and phenotypic data can then be used by the curator in making decisions about eliminating unwanted duplicates.

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Rationale

~ Eliminating unintentional duplication of germplasm in genebanks will allow more resources to be devoted towards acquiring new material, characterizing accessions, and routine regenerations.

~ Based on passport data, we suspect that 15% or more of the 6,000 accessions of tomato at the Plant Genetic Resources Unit may be unwanted duplicates. Plants that are identical in appearance are not necessarily genetically the same.

~ In a pilot study to estimate redundancy, two heirloom tomato cultivars were assessed for molecular genetic variation within and among accessions. Two plants from each of six accessions of San Marzano and six accessions of Globe were genotyped at eight microsatellite loci distributed across the genome.

~ Results from this study will be used to design a sampling strategy to genotype the 200-300 accessions of American Heirloom tomatoes in the Plant Genetic Resources Unit's collection.

Table 1. Tomato accessions genotyped and phenotyped in this study.

Entry	Name	Accession	Cultivar
1	San Marzano 1	14594	San Marzano
2	San Marzano 2	32287	"
3	San Marzano 3	128990	"
4	San Marzano 4	212417	"
5	San Marzano 5	212418	"
6	San Marzano 6	303786	"
7	Hoffman Globe A	254659	Globe
8	Globe Association	270185	"
9	Globe Livingston	270186	"
10	Globe Strain A	270187	"
11	Growthens Globe	270189	"
12	College Globe	407440	"

Table 2. AMOVA of San Marzano versus Globe tomato cultivars based on eight SSR loci^a.

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation	P-value
Among cultivars	1	156.509	6.31890	67.51	0.003
Among accessions within cultivars	10	111.970	2.89402	30.92	0.000
Within accessions	34	5.000	0.14706	1.57	0.000
Total	45	273.478	9.35998		

^a TMS56, TMS1, TMS26, EST253712, TMS29, TMS34, TMS4, TMS42.

Fig. 1. UPGMA dendrogram based on alleles at eight SSR loci for 12 tomato accessions.

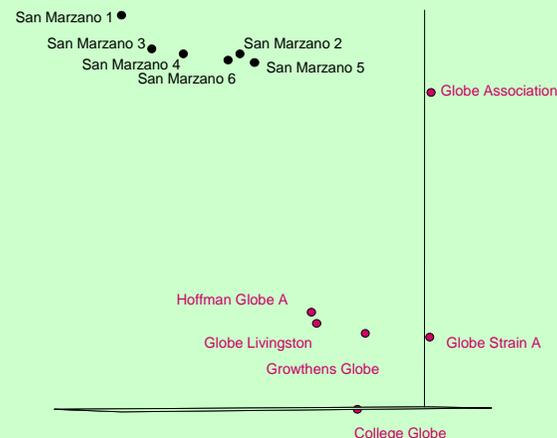
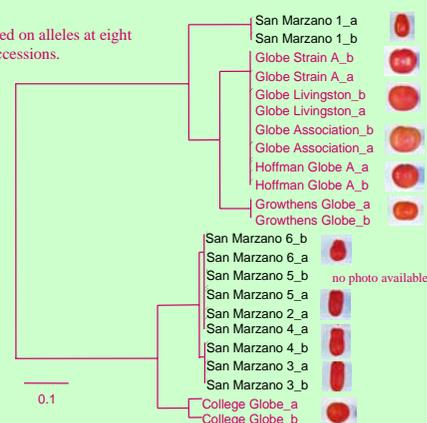


Fig. 2. Principle components analysis of 12 tomato accessions based on 22 phenotypic traits. (growth habit, canopy size, flowers per inflorescence, maturity, leaf type, inflorescence type, fruit set no., ext. color imm. fruit, ext. appear. mature fruit, shoulder color, int. flesh color mat. fruit, mat. fruit int. color intensity, fruit shape, pistil scar, ext. color mat. fruit, fruit firmness, nipped fruit, jointless, radial cracking, concentric cracking, cuticle cracking, uniformity of fruit size).

Conclusions

~ AMOVA results showed that 30.92% of the total molecular genetic variation was found among accessions within cultivars (Table 2). We found one accession out of six for each cultivar, San Marzano and Globe, to be genotypically differentiated at these loci (Fig. 1).

~ Genotypically differentiated accessions may appear similar phenotypically, e.g., San Marzano 1 versus San Marzano 2 through 6 (Figs. 1 and 2).

~ Accessions that were genotypically identical at these eight loci could be differentiated phenotypically, e.g., Globe Association (Figs. 1 and 2).

~ Phenotypic and molecular evidence must be considered together when estimating duplication in germplasm collections.

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